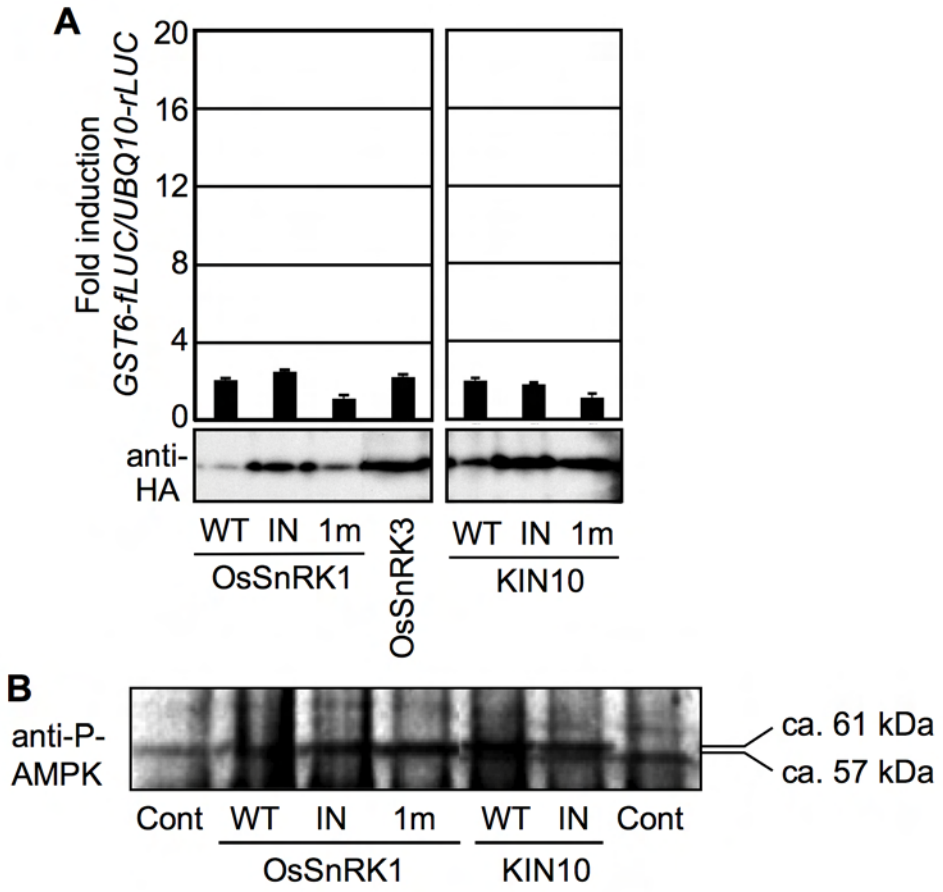
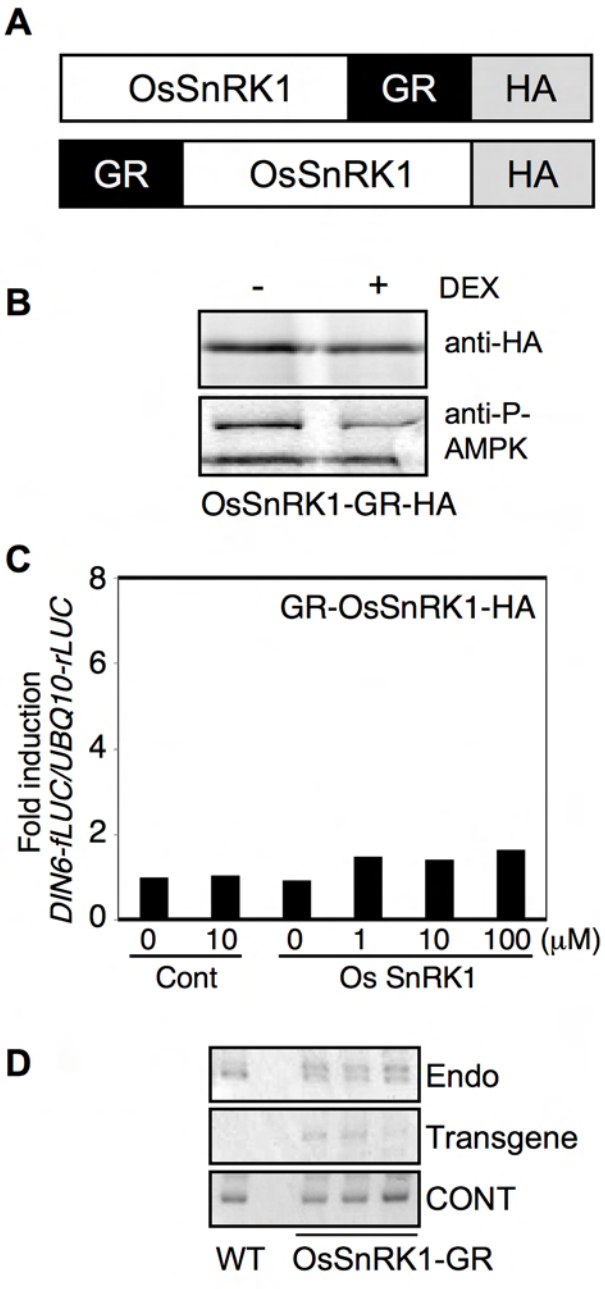
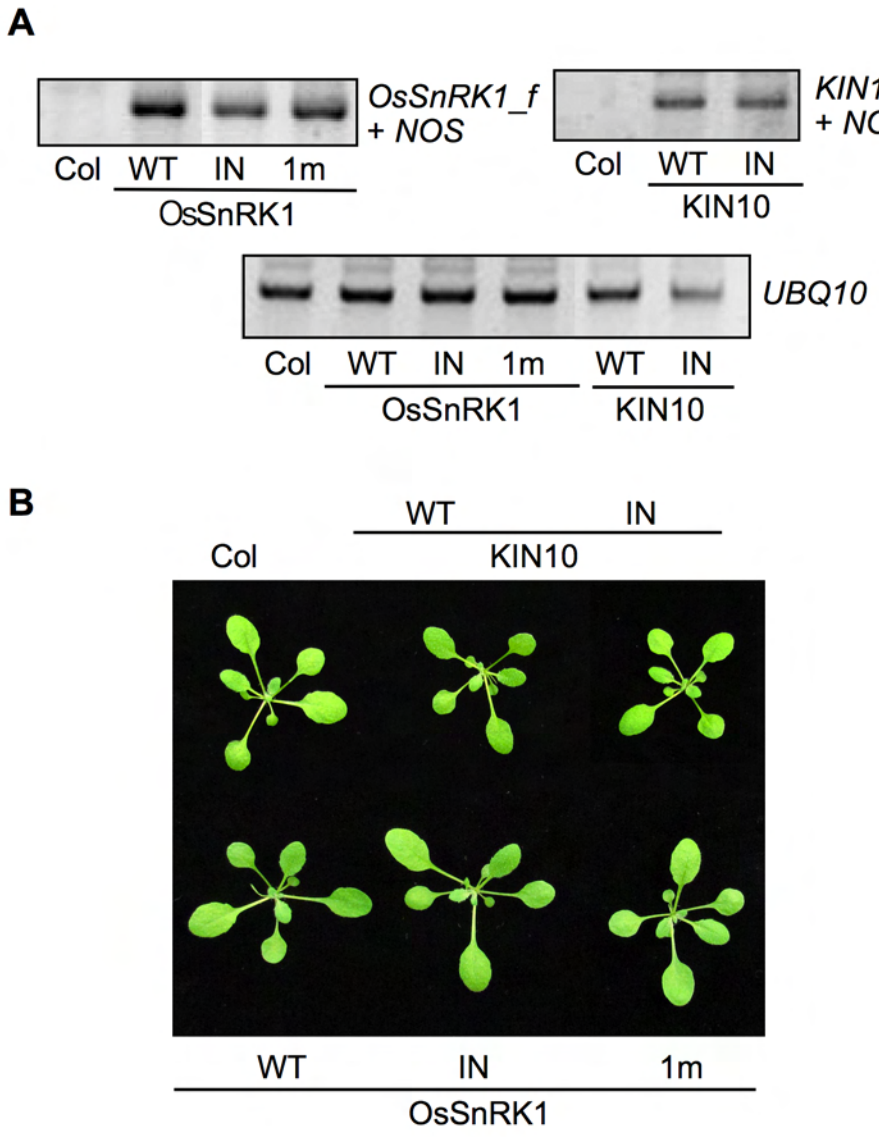


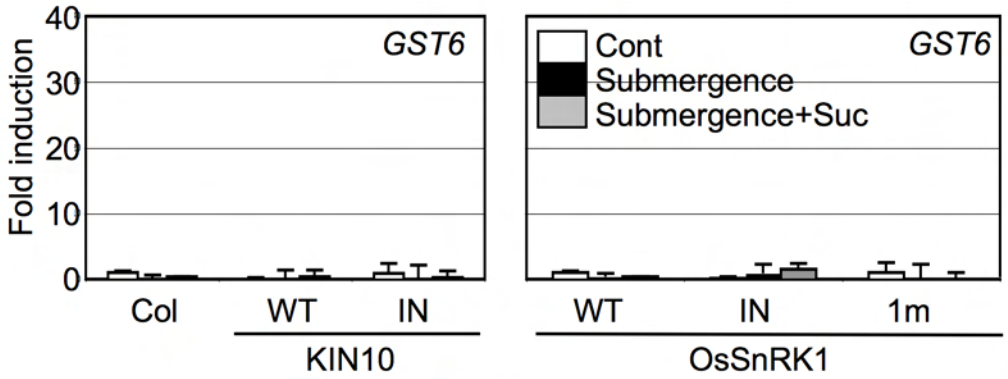
Supplemental Figure S1. Plant SnRK1 did not activate a general stress-responsive *GST6* promoter activity. A, Reporter activities of GST6-fLUC were measured upon expression of WT or inactive forms of SnRK1. Inactive forms were ATP-binding site (IN)- and catalytic site (1m)-mutated SnRK1s. Protoplasts were cotransfected with a designated effector, *GST6-fLUC* and *UBQ10-rLUC* constructs. UBQ10 promoter activity served as transfection control. HA-tagged SnRK1 expression was shown by protein blot analysis using anti-HA antibody. B, The phosphorylation of *OsSnRK1, KIN10* and their mutated forms were detected by protein blot analysis by using anti-phospho-AMPKα antibody.


A
OsSnRK1
GR
HA
GR
OsSnRK1
HA
B
-
+
DEX
anti-HA
anti-P-AMPK
OsSnRK1-GR-HA
C
GR-OsSnRK1-HA
Fold induction
DIN6-fLUC/UBQ10-rLUC
8
6
4
2
0
0
10
0
1
10
100
(μM)
Cont
Os SnRK1
D
Endo
Transgene
CONT
WT
OsSnRK1-GR

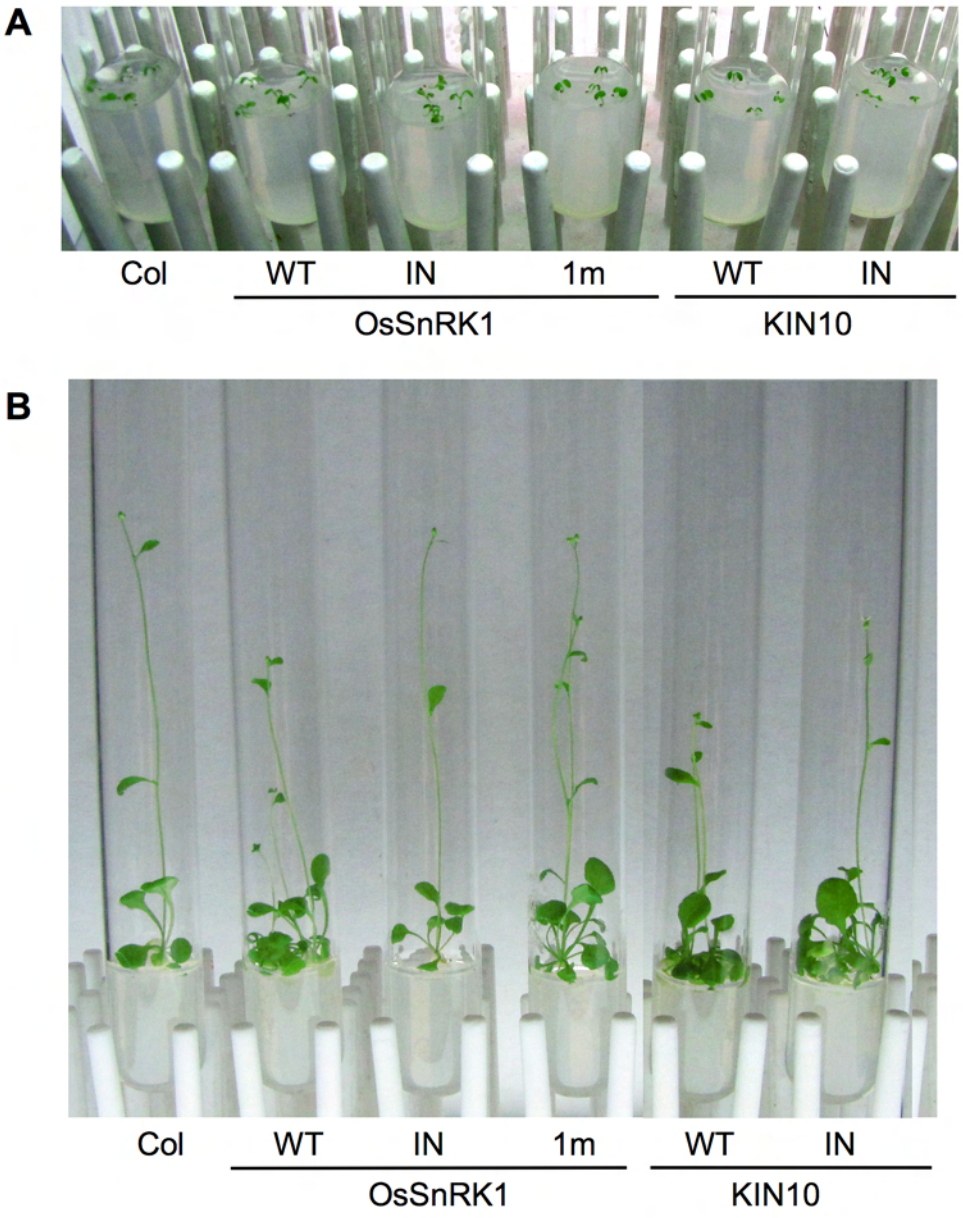
Supplemental Figure S2. SnRK1 localized in the nucleus and affected gene expression. A, Schematic diagrams of glucocorticoid receptor (GR), OsSnRK1 and hemagglutinin epitope (HA) fusion constructs. B, Protein abundance and phosphorylation of the T-loop of OsSnRK1-GR-HA were detected by protein blot analysis using anti-HA and anti-phospho-AMPKα antibody, respectively. C, Even with DEX treatment, GR-OsSnRK1-HA could not activate DIN6-LUC reporter. The experiments were repeated twice with consistent results. The means of triplicate measurements were shown with standard error bars. D, Transcript abundance of endogenous and *SnRK1-GR* transgenic plants was determined by using semi-quantitative RT-PCR. *UBQ10* served as an internal control.



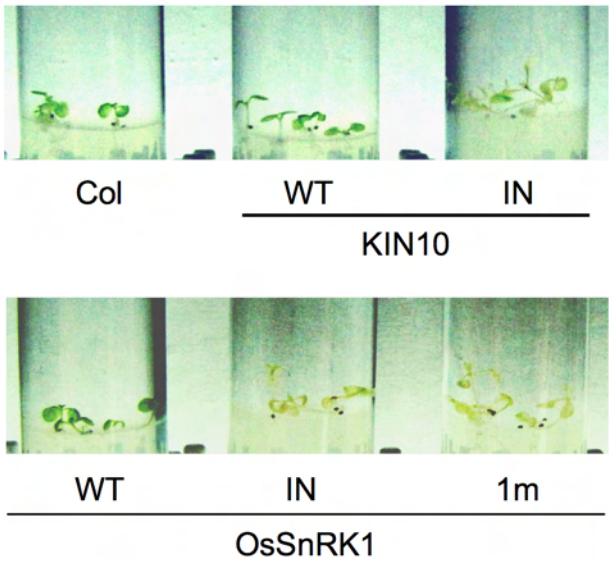
Supplemental Figure S3. Transcript abundance of *OsSnRK1, KIN10,* and their mutated forms in stably transformed Arabidopsis transgenic plants. A, Transcript abundance was determined by using semi-quantitative RT-PCR. *UBQ10* served as an internal control. B, *SnRK1* transgenic plants grew normally in soil at 23°C under a 16 h photoperiod (60 $\mu molm^{-2}s^{-1}$).



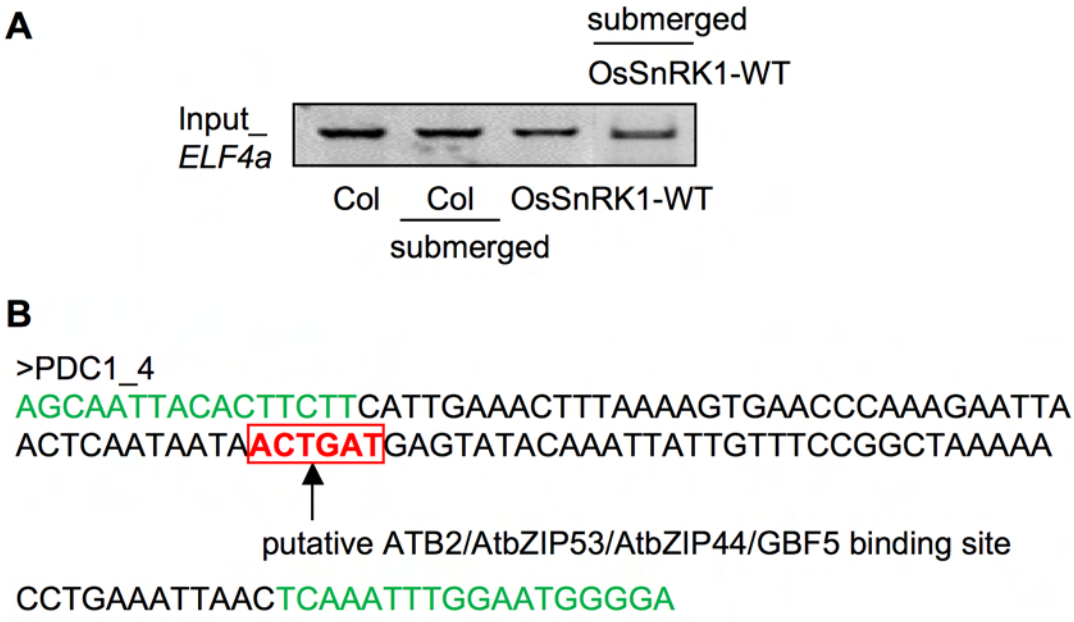
Supplemental Figure S4. The *GST6* gene expression was not induced by OsSnRK1 or KIN10 under flooding. Gene expression was measured by using real time RT-PCR. RNA was extracted from Col as well as transgenic plants expressing WT and inactive forms of *OsSnRK1* or *KIN10* under the flooding condition (24 h) in the absence or presence of 90 mM sucrose.



Supplemental Figure S5. Col and transgenic plants expressing WT and inactive forms of *OsSnRK1* and *KIN10* showed similar seedling growth in A, 3 d and B, 30 d after germination. Plants were grown inside of 30 ml test tube holding 5 ml of MS agar medium containing 0.5% sucrose under a photoperiod of 16 h light/8 h dark (50 $\mu molm^{-2}s^{-1}$) at 23°C. Seeds were stratified at 4°C for 4 d before plating.



Supplemental Figure S6. Detailed photo of Col and *SnRK1* expressing transgenic seedling development under flooding. Col as well as transgenic seedlings expressing WT forms of SnRK1 maintained green leaves during prolonged flooding conditions in the dark. Experiments repeated three times with triplicates and showed consistent results.



Supplemental Figure S7. For the comparison of SnRK1-DNA association with and without submergence. A, PCR product before ChIP was shown as input controls. B, DNA sequences of PDC1_4 were shown. A well conserved putative ATB2/AtbZIP53/AtbZIP44/GBF5 binding site was shown in red and a specific primer set for this region was shown in green.

Supplemental Table S1. Oligonucleotides for qRT-PCR.

Oligo name	Oligonucleotide (5′ - 3′)
ADH1_f:	TTGCTCCACCGCAGAAACAC
ADH1_r:	CCAACACTCTCAACAATCCCTCC
CYP94B3_f:	CGGGAAGAGATACAACGTCAG
CYP94B3_r:	GTCATCGTTCTCAGTCAACA
DIN1_f:	CAGAGTCGGATCAGGAATGG
DIN1_r:	ATTTGACCGCTCTCACAACC
DIN6_f:	AACTTGTCGCCAGATCAAGG
DIN6_r:	GGAACACGTGCCTCTAGTCC
GST6_f:	CGCGTCCTCGCTACTCTTTAC
GST6_r:	GAGCAGGAATTTGACCGAAG
PDC1_f:	TGATGCTTCAGGCTATGCTTT
PDC1_r:	GTTGAAGATTGGACCTGCAAA
TCH4_f:	TGAAGCTTGTCCCTGGAAAC
TCH4_r:	GCCTTGTGTGTAGACATTTGTGTG
ELF4a_f:	TCATAGATCTGGTCCTTGAAAC
ELF4a_r:	GGCAGTCTCTTCGTG CTGAC
Tubulin4_f:	AGGGAAAGGAAGAGAGGAAG
Tubulin4_r:	GCTGGCTAATCCTACCTTTGG
UBQ10_f:	AGATCCAGGACAAGGAGGTATTC
UBQ10_r:	CGCAGGACCAAGTGAAGAGTAG
*ADH1_6*f:	CTTCTTCCAATTACCAGCTGC
*ADH1_6*r:	AAAAAGAAAACCTTTGCATCG
*PDC1_4*f:	AGCAATTACACTTCTTCATTGAAACTT
*PDC1_4*r:	CCCCATTCCAAATTTGAGTTA